

Serial Number:

09/990,385

070

01PE

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

ENTERED☐Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☐Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____☐

Inserted mandatory headings, specifically: _____

☐

Corrected an obvious error in the response, specifically: _____

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically: _____

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____☒

Other:

Corrected the misalignment of amino acid number.

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/990,385

DATE: 12/03/2001

TIME: 14:31:03

Input Set : A:\yanai sequence listing.txt

Output Set: N:\CRF3\11212001\I990385.raw

Does Not Comply
Corrected Diskette Needed

error on p. 4

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Koji YANAI et al.
6 (ii) TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
7 ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR
PRODUCING
8 BETA-FRUCTOFURANOSIDASE, AND BETA-FRUCTOFURANOSIDASE
VARIANT
9 (iii) NUMBER OF SEQUENCES: 35
10 (iv) CORRESPONDENCE ADDRESS:
11 (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
12 (B) STREET: 2033 K Street, N.W., Suite 800
13 (C) CITY: Washington
14 (D) STATE: D.C.
15 (E) COUNTRY: U.S.A.
16 (F) ZIP: 20006
17 (v) COMPUTER READABLE FORM:
18 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
19 (B) COMPUTER: IBM Compatible
20 (C) OPERATING SYSTEM: MS-DOS
21 (D) SOFTWARE: Wordperfect 5.1
22 (vi) CURRENT APPLICATION DATA:
C--> 23 (A) APPLICATION NUMBER: US/09/990,385
C--> 24 (B) FILING DATE: 23-Nov-2001
25 (vii) PRIOR APPLICATION DATA:
26 (A) APPLICATION NUMBER: 09/142,623
27 (B) FILING DATE: September 10, 1998
28 (viii) ATTORNEY/AGENT INFORMATION:
29 (A) NAME: Lee Cheng
30 (B) REGISTRATION NUMBER: 40,949
31 (C) REFERENCE/DOCKET NUMBER: 2001-1611
32 (ix) TELECOMMUNICATION INFORMATION:
33 (A) TELEPHONE: 202-721-8200
34 (B) TELEFAX: 202-721-8250

ERRORED SEQUENCES

35 (2) INFORMATION FOR SEQ ID NO: 1:
36 (i) SEQUENCE CHARACTERISTICS:
37 (A) LENGTH: 635 amino acid residues
38 (B) TYPE: amino acid
39 (C) STRANDEDNESS: Not relevant
W--> 40 (D) TOPOLOGY: Not relevant
41 (ii) MOLECULE TYPE: protein
42 (vi) ORIGINAL SOURCE:
43 (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
44 (ATCC 20611)

45 (ix) FEATURE:

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```

46      (A) NAME/KEY: mat peptide
47      (B) LOCATION: 1..635
48      (C) IDENTIFICATION METHOD: E
49      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
50 Ser Tyr His Leu Asp Thr Thr Ala Pro Pro Pro Thr Asn Leu Ser Thr
51 1      5      10      15
52 Leu Pro Asn Asn Thr Leu Phe His Val Trp Arg Pro Arg Ala His Ile
53      20      25      30
54 Leu Pro Ala Glu Gly Gln Ile Gly Asp Pro Cys Ala His Tyr Thr Asp
55      35      40      45
56 Pro Ser Thr Gly Leu Phe His Val Gly Phe Leu His Asp Gly Asp Gly
57      50      55      60
58 Ile Ala Gly Ala Thr Thr Ala Asn Leu Ala Thr Tyr Thr Asp Thr Ser
59 65      70      75      80
60 Asp Asn Gly Ser Phe Leu Ile Gln Pro Gly Gly Lys Asn Asp Pro Val
61      85      90      95
62 Ala Val Phe Asp Gly Ala Val Ile Pro Val Gly Val Asn Asn Thr Pro
63      100     105     110
64 Thr Leu Leu Tyr Thr Ser Val Ser Phe Leu Pro Ile His Trp Ser Ile
65      115     120     125
66 Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ala Arg Asp
67      130     135     140
68 Gly Gly Arg Arg Phe Asp Lys Leu Asp Gln Gly Pro Val Ile Ala Asp
69 145     150     155     160
70 His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro Phe Val Phe
71      165     170     175
72 Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu Glu Val Ala
73      180     185     190
74 Arg Asn Glu Thr Ala Val Gln Gln Ala Val Asp Gly Trp Thr Glu Lys
75      195     200     205
76 Asn Ala Pro Trp Tyr Val Ala Val Ser Gly Gly Val His Gly Val Gly
77      210     215     220
78 Pro Ala Gln Phe Leu Tyr Arg Gln Asn Gly Gly Asn Ala Ser Glu Phe
79 225     230     235     240
80 Gln Tyr Trp Glu Tyr Leu Gly Glu Trp Trp Gln Glu Ala Thr Asn Ser
81      245     250     255
82 Ser Trp Gly Asp Glu Gly Thr Trp Ala Gly Arg Trp Gly Phe Asn Phe
83      260     265     270
84 Glu Thr Gly Asn Val Leu Phe Leu Thr Glu Glu Gly His Asp Pro Gln
85      275     280     285
86 Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser Gly Leu Pro
87      290     295     300
88 Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp Ala Ala Gly
89 305     310     315     320
90 Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val Glu Phe Ser
91      325     330     335
92 Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala Tyr Ala Ala
93      340     345     350
94 Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys Thr Ser Gly

```

RAW SEQUENCE LISTING

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```

95          355          360          365
96 Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr Gly Asp Gln
97          370          375          380
98 Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly Trp Thr Gly
99 385          390          395          400
100 Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val Glu Asn Val
101          405          410          415
102 Val Asp Asn Glu Leu Val Arg Glu Glu Gly Val Ser Trp Val Val Gly
103          420          425          430
104 Glu Ser Asp Asn Gln Thr Ala Arg Leu Arg Thr Leu Gly Ile Thr Ile
105          435          440          445
106 Ala Arg Glu Thr Lys Ala Ala Leu Leu Ala Asn Gly Ser Val Thr Ala
107          450          455          460
108 Glu Glu Asp Arg Thr Leu Gln Thr Ala Ala Val Val Pro Phe Ala Gln
109 465          470          475          480
110 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Gln Leu Glu Phe Pro
111          485          490          495
112 Ala Ser Ala Arg Ser Ser Pro Leu Gln Ser Gly Phe Glu Ile Leu Ala
E--> 113          500          505          510
114 Ser Glu Leu Glu Arg Thr Ala Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
115          515          520          525
116 Leu Val Val Asp Arg Ser Gln Thr Ser Ala Ala Ala Pro Thr Asn Pro
117          530          535          540
118 Gly Leu Asp Ser Phe Thr Glu Ser Gly Lys Leu Arg Leu Phe Asp Val
119 545          550          555          560
120 Ile Glu Asn Gly Gln Glu Gln Val Glu Thr Leu Asp Leu Thr Val Val
121          565          570          575
122 Val Asp Asn Ala Val Val Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu
123          580          585          590
124 Ser Thr Trp Ala Arg Ser Trp Tyr Asp Asn Ser Thr Gln Ile Arg Phe
125          595          600          605
126 Phe His Asn Gly Glu Gly Glu Val Gln Phe Arg Asn Val Ser Val Ser
127          610          615          620
128 Glu Gly Leu Tyr Asn Ala Trp Pro Glu Arg Asn
129 625          630          635

```

—misaligned numbering
note: pls. use spacebar
instead of tab key

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/990,385

DATE: 12/03/2001

TIME: 14:31:04

Input Set : A:\yanai sequence listing.txt

Output Set: N:\CRF3\11212001\I990385.raw

L:23 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:24 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:40 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:113 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:269 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:279 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:354 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11
L:485 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:617 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:627 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:637 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:647 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:657 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:667 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:677 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:687 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:697 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:717 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:727 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:737 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:747 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:757 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:767 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:777 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:787 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:797 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:807 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:817 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35